



SEQUENCE LISTING

<110> MACK, DAVID
GISH, KURT

<120> NOVEL METHODS OF DIAGNOSING AND TREATING BREAST CANCER,
COMPOSITIONS, AND METHODS OF SCREENING FOR BREAST
CANCER MODULATORS

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<141> 2000-03-15

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<150> US 09/450,810

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<150> US 09/439,878

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<210> 12

<211> 582

<212> DNA

<213> Homo sapiens

<400> 12

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<210> 13

<211> 193

<212> PRT

<213> Homo sapiens

<400> 13

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Arg Gly Trp Leu Gln Ser Ser Asp His Gly Gln Thr Ser Ser Leu Trp
35 40 45
Trp Lys Cys Ser Gln Glu Gly Gly Gly Ser Gly Ser Tyr Glu Glu Gly
50 55 60
Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg Ala Ala Ala Met
65 70 75 80
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85 90 95
Phe Ala Leu Cys Gly Pro Gln Met Leu Val Phe Leu Arg Val Ile Gly
100 105 110
Gly Leu Leu Ala Leu Ala Ala Val Phe Gln Ile Leu Ser Leu Val Ile
115 120 125
Tyr Pro Val Lys Tyr Thr Gln Thr Phe Thr Leu His Ala Asn Pro Ala
130 135 140
Val Thr Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr
145 150 155 160
Ile Ile Leu Ile Gly Cys Ala Phe Phe Phe Cys Cys Leu Pro Asn Tyr
165 170 175
Glu Asp Asp Leu Leu Gly Asn Ala Lys Pro Arg Tyr Phe Tyr Thr Ser
180 185 190
Ala

<210> 14

<211> 193

<212> PRT

<213> Mouse

<400> 14

Met Leu Arg Cys Gly Leu Ala Cys Glu Arg Cys Arg Trp Ile Leu Pro
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Arg Gly Trp Leu Gln Ser Ser Asn His Ile Gln Thr Ser Ser Leu Trp
35 40 45
Trp Arg Cys Phe Asp Glu Gly Gly Gly Ser Gly Ser Tyr Asp Asp Gly
50 55 60

Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg Ala Ala Ala Ala Thr
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 85 90 95
 Phe Ala Leu Cys Gly Pro Met Gln Leu Val Phe Leu Arg Val Ile Gly
 100 105 110
 Gly Leu Leu Ala Leu Ala Ala Ile Phe Gln Ile Leu Ser Leu Val Ile
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 Tyr Pro Val Lys Tyr Thr Gln Thr Phe Arg Leu His Asp Asn Pro Ala
 130 135 140
 Val Asn Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr
 145 150 155 160
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 Glu Asp Asp Leu Leu Gly Ala Ala Lys Pro Arg Tyr Phe Tyr Pro Pro
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Ala

<210> 15
 <211> 124
 <212> PRT
 <213> Rat

<400> 15

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 Pro Gln Met Leu Val Phe Leu Arg Val Ile Gly Gly Leu Leu Ala Leu
 35 40 45
 Ala Ala Val Phe Gln Ile Ile Ser Leu Val Ile Tyr Pro Val Lys Tyr
 50 55 60
 Thr Gln Thr Phe Arg Leu His Asp Asn Pro Ala Val Asn Tyr Ile Tyr
 65 70 75 80
 Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr Ile Ile Leu Ile Gly
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<210> 16
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

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 1 5 10 15

<210> 17
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 17
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 1 5 10 15

<210> 18
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 18
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 1 5 10 15

<210> 19
 <211> 1970
 <212> DNA
 <213> Mouse

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 cgctgcggcc tggcctgcga gcgctgcagg tggatcctgc ccctgctgct gctcagcgcc 240
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<210> 20
 <211> 582
 <212> DNA
 <213> Mouse

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<210> 21
 <211> 536
 <212> DNA
 <213> Rat

<400> 21						
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<210> 22
 <211> 375
 <212> DNA
 <213> Rat

<400> 22
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<210> 23
<211> 471
<212> DNA
<213> Homo sapiens

<400> 23
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ttcatgcttc ctgtgatctt atccaactac ttactctgac tacgatattc cctttatctc 420
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<210> 24
<211> 273
<212> DNA
<213> Homo sapiens

<400> 24
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gccctgatg ctgaaaccac tgctgctgca accactgcca ccaactgctgc tcctaccact 180
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<210> 25
<211> 90
<212> PRT
<213> Homo sapiens

<400> 25
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Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu Thr Thr Ala
35 40 45
Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr Ala Thr Thr Ala
50 55 60
Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val Leu Pro Lys Trp Val
65 70 75 80

Gly Asp Leu Pro Asn Gly Arg Val Cys Pro
85 90

<210> 26
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 26
Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr Tyr Pro Ala Cys
1 5 10 15

<210> 27
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 27
Leu Pro Lys Trp Val Gly Asp Leu Pro Asn Gly Arg Val Cys Pro
1 5 10 15

<210> 28
<211> 1555
<212> DNA
<213> Homo sapiens

<400> 28
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Ser Glu Val Gly Leu Leu Lys Asn Ala Glu Arg Glu Gln Glu Ser Glu
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Glu Glu Met
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<210> 30
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 30
 Tyr Pro Pro Ser Gly Gly Pro Ala Trp Asp Leu Met Asp His Cys
 1 5 10 15

<210> 31
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 31
 Cys Leu Lys Asn Ala Glu Arg Glu Gln Glu Ser Glu Glu Glu Met
 1 5 10 15

<210> 32
 <211> 10320
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> (10123)..(10185)
 <223> "n" at positions 10123 and 10185 can be any base.

<400> 32
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<210> 35
 <211> 871
 <212> PRT
 <213> Homo sapiens

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Leu Leu Gly Ser Leu Cys Ser Thr Val Arg Ser Pro Arg Phe Arg Gly
      20              25              30

Arg Ile Gln Gln Glu Arg Lys Asn Ile Arg Pro Asn Ile Ile Leu Val
      35              40              45

Leu Thr Asp Asp Gln Asp Val Glu Leu Gly Ser Leu Gln Val Met Asn
 50              55              60

Lys Thr Arg Lys Ile Met Glu His Gly Gly Ala Thr Phe Ile Asn Ala
 65              70              75              80

Phe Val Thr Thr Pro Met Cys Cys Pro Ser Arg Ser Ser Met Leu Thr
      85              90              95

Gly Lys Tyr Val His Asn His Asn Val Tyr Thr Asn Asn Glu Asn Cys
 100              105              110

Ser Ser Pro Ser Trp Gln Ala Met His Glu Pro Arg Thr Phe Ala Val
 115              120              125

Tyr Leu Asn Asn Thr Gly Tyr Arg Thr Ala Phe Phe Gly Lys Tyr Leu
 130              135              140

Asn Glu Tyr Asn Gly Ser Tyr Ile Pro Pro Gly Trp Arg Glu Trp Leu
 145              150              155              160

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Gly Leu Ile Lys Asn Ser Arg Phe Tyr Asn Tyr Thr Val Cys Arg Asn
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 Gly Ile Lys Glu Lys His Gly Phe Asp Tyr Ala Lys Asp Tyr Phe Thr
 180 185 190
 Asp Leu Ile Thr Asn Glu Ser Ile Asn Tyr Phe Lys Met Ser Lys Arg
 195 200 205
 Met Tyr Pro His Arg Pro Val Met Met Val Ile Ser His Ala Ala Pro
 210 215 220
 His Gly Pro Glu Asp Ser Ala Pro Gln Phe Ser Lys Leu Tyr Pro Asn
 225 230 235 240
 Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn Met Asp
 245 250 255
 Lys His Trp Ile Met Gln Tyr Thr Gly Pro Met Leu Pro Ile His Met
 260 265 270
 Glu Phe Thr Asn Ile Leu Gln Arg Lys Arg Leu Gln Thr Leu Met Ser
 275 280 285
 Val Asp Asp Ser Val Glu Arg Leu Tyr Asn Met Leu Val Glu Thr Gly
 290 295 300
 Glu Leu Glu Asn Thr Tyr Ile Ile Tyr Thr Ala Asp His Gly Tyr His
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 Ile Gly Gln Phe Gly Leu Val Lys Gly Lys Ser Met Pro Tyr Asp Phe
 325 330 335
 Asp Ile Arg Val Pro Phe Phe Ile Arg Gly Pro Ser Val Glu Pro Gly
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 Ser Ile Val Pro Gln Ile Val Leu Asn Ile Asp Leu Ala Pro Thr Ile
 355 360 365
 Leu Asp Ile Ala Gly Leu Asp Thr Pro Pro Asp Val Asp Gly Lys Ser
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 Val Leu Lys Leu Leu Asp Pro Glu Lys Pro Gly Asn Arg Phe Arg Thr
 385 390 395 400
 Asn Lys Lys Ala Lys Ile Trp Arg Asp Thr Phe Leu Val Glu Arg Gly
 405 410 415
 Lys Phe Leu Arg Lys Lys Glu Glu Ser Ser Lys Asn Ile Gln Gln Ser
 420 425 430
 Asn His Leu Pro Lys Tyr Glu Arg Val Lys Glu Leu Cys Gln Gln Ala
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 Arg Tyr Gln Thr Ala Cys Glu Gln Pro Gly Gln Lys Trp Gln Cys Ile
 450 455 460
 Glu Asp Thr Ser Gly Lys Leu Arg Ile His Lys Cys Lys Gly Pro Ser
 465 470 475 480

Asp Leu Leu Thr Val Arg Gln Ser Thr Arg Asn Leu Tyr Ala Arg Gly
 485 490 495
 Phe His Asp Lys Asp Lys Glu Cys Ser Cys Arg Glu Ser Gly Tyr Arg
 500 505 510
 Ala Ser Arg Ser Gln Arg Lys Ser Gln Arg Gln Phe Leu Arg Asn Gln
 515 520 525
 Gly Thr Pro Lys Tyr Lys Pro Arg Phe Val His Thr Arg Gln Thr Arg
 530 535 540
 Ser Leu Ser Val Glu Phe Glu Gly Glu Ile Tyr Asp Ile Asn Leu Glu
 545 550 555 560
 Glu Glu Glu Glu Leu Gln Val Leu Gln Pro Arg Asn Ile Ala Lys Arg
 565 570 575
 His Asp Glu Gly His Lys Gly Pro Arg Asp Leu Gln Ala Ser Ser Gly
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 Gly Asn Arg Gly Arg Met Leu Ala Asp Ser Ser Asn Ala Val Gly Pro
 595 600 605
 Pro Thr Thr Val Arg Val Thr His Lys Cys Phe Ile Leu Pro Asn Asp
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 Ser Ile His Cys Glu Arg Glu Leu Tyr Gln Ser Ala Arg Ala Trp Lys
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 Asp His Lys Ala Tyr Ile Asp Lys Glu Ile Glu Ala Leu Gln Asp Lys
 645 650 655
 Ile Lys Asn Leu Arg Glu Val Arg Gly His Leu Lys Arg Arg Lys Pro
 660 665 670
 Glu Glu Cys Ser Cys Ser Lys Gln Ser Tyr Tyr Asn Lys Glu Lys Gly
 675 680 685
 Val Lys Lys Gln Glu Lys Leu Lys Ser His Leu His Pro Phe Lys Glu
 690 695 700
 Ala Ala Gln Glu Val Asp Ser Lys Leu Gln Leu Phe Lys Glu Asn Asn
 705 710 715 720
 Arg Arg Arg Lys Lys Glu Arg Lys Glu Lys Arg Arg Gln Arg Lys Gly
 725 730 735
 Glu Glu Cys Ser Leu Pro Gly Leu Thr Cys Phe Thr His Asp Asn Asn
 740 745 750
 His Trp Gln Thr Ala Pro Phe Trp Asn Leu Gly Ser Phe Cys Ala Cys
 755 760 765
 Thr Ser Ser Asn Asn Asn Thr Tyr Trp Cys Leu Arg Thr Val Asn Glu
 770 775 780
 Thr His Asn Phe Leu Phe Cys Glu Phe Ala Thr Gly Phe Leu Glu Tyr
 785 790 795 800

Phe Asp Met Asn Thr Asp Pro Tyr Gln Leu Thr Asn Thr Val His Thr
805 810 815

Val Glu Arg Gly Ile Leu Asn Gln Leu His Val Gln Leu Met Glu Leu
820 825 830

Arg Ser Cys Gln Gly Tyr Lys Gln Cys Asn Pro Arg Pro Lys Asn Leu
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Asp Val Gly Asn Lys Asp Gly Gly Ser Tyr Asp Leu His Arg Gly Gln
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Leu Trp Asp Gly Trp Glu Gly
865 870

<210> 36
<211> 1922
<212> DNA
<213> Homo sapiens

<400> 36
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aa 1922

<210> 37
<211> 1179

<212> DNA
 <213> Homo sapiens

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<210> 38
 <211> 392
 <212> PRT
 <213> Homo sapiens

<220>
 <221> UNSURE
 <222> (111)
 <223> "Xaa" at position 111 can be any amino acid.

<400> 38
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 35 40 45
 Leu Cys Pro Asn Gly Thr Phe Gln Asn Glu Glu Gly Gln Met Thr Cys
 50 55 60
 Glu Pro Cys Pro Arg Pro Gly Asn Ser Gly Ala Leu Lys Thr Pro Glu
 65 70 75 80
 Ala Trp Asn Met Ser Glu Cys Gly Gly Leu Cys Gln Pro Thr Glu Tyr
 85 90 95
 Ser Ala Asp Gly Phe Ala Pro Cys Gln Leu Cys Ala Leu Gly Xaa Phe
 100 105 110
 Gln Pro Glu Ala Gly Arg Thr Ser Cys Phe Pro Cys Gly Gly Gly Leu
 115 120 125

Ala Thr Lys His Gln Gly Ala Thr Ser Phe Gln Asp Cys Glu Thr Arg
 130 135 140
 Val Gln Cys Ser Pro Gly His Phe Tyr Asn Thr Thr Thr His Arg Cys
 145 150 155 160
 Ile Arg Cys Pro Val Gly Thr Tyr Gln Pro Glu Phe Gly Lys Asn Asn
 165 170 175
 Cys Val Ser Cys Pro Gly Asn Thr Thr Thr Asp Phe Asp Gly Ser Thr
 180 185 190
 Asn Ile Thr Gln Cys Lys Asn Arg Arg Cys Gly Gly Glu Leu Gly Asp
 195 200 205
 Phe Thr Gly Tyr Ile Glu Ser Pro Asn Tyr Pro Gly Asn Tyr Pro Ala
 210 215 220
 Asn Thr Glu Cys Thr Trp Thr Ile Asn Pro Pro Pro Lys Arg Arg Ile
 225 230 235 240
 Leu Ile Val Val Pro Glu Ile Phe Leu Pro Ile Glu Asp Asp Cys Gly
 245 250 255
 Asp Tyr Leu Val Met Arg Lys Thr Ser Ser Ser Asn Ser Val Thr Thr
 260 265 270
 Tyr Glu Thr Cys Gln Thr Tyr Glu Arg Pro Ile Ala Phe Thr Ser Arg
 275 280 285
 Ser Lys Lys Leu Trp Ile Gln Phe Lys Ser Asn Glu Gly Asn Ser Ala
 290 295 300
 Arg Gly Phe Gln Val Pro Tyr Val Thr Tyr Asp Glu Asp Tyr Gln Glu
 305 310 315 320
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 His Gln Glu Ile Leu Lys Asp Lys Lys Leu Ile Lys Ala Leu Phe Asp
 340 345 350
 Val Leu Ala His Pro Gln Asn Tyr Phe Lys Tyr Thr Ala Gln Glu Ser
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 Arg Glu Met Phe Pro Arg Ser Phe Ile Arg Leu Leu Arg Ser Lys Val
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 Ser Arg Phe Leu Arg Pro Tyr Lys
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<210> 39
 <211> 392
 <212> PRT
 <213> Homo sapiens

<220>
 <221> UNSURE

<222> (111)

<223> "Xaa" at position 111 can be any amino acid.

<400> 39

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			20					25					30			
Ser	Cys	Arg	Ala	Gly	Thr	Tyr	Tyr	Asp	Gly	Ala	Arg	Glu	Arg	Cys	Ile	
		35					40					45				
Leu	Cys	Pro	Asn	Gly	Thr	Phe	Gln	Asn	Glu	Glu	Gly	Gln	Met	Thr	Cys	
	50					55					60					
Glu	Pro	Cys	Pro	Arg	Pro	Gly	Asn	Ser	Gly	Ala	Leu	Lys	Thr	Pro	Glu	
65					70					75					80	
Ala	Trp	Asn	Met	Ser	Glu	Cys	Gly	Gly	Leu	Cys	Gln	Pro	Thr	Glu	Tyr	
				85					90					95		
Ser	Ala	Asp	Gly	Phe	Ala	Pro	Cys	Gln	Leu	Cys	Ala	Leu	Gly	Xaa	Phe	
			100					105					110			
Gln	Pro	Glu	Ala	Gly	Arg	Thr	Ser	Cys	Phe	Pro	Cys	Gly	Gly	Gly	Leu	
		115					120					125				
Ala	Thr	Lys	His	Gln	Gly	Ala	Thr	Ser	Phe	Gln	Asp	Cys	Glu	Thr	Arg	
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Val	Gln	Cys	Ser	Pro	Gly	His	Phe	Tyr	Asn	Thr	Thr	Thr	His	Arg	Cys	
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Ile	Arg	Cys	Pro	Val	Gly	Thr	Tyr	Gln	Pro	Glu	Phe	Gly	Lys	Asn	Asn	
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Cys	Val	Ser	Cys	Pro	Gly	Asn	Thr	Thr	Thr	Asp	Phe	Asp	Gly	Ser	Thr	
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Asn	Ile	Thr	Gln	Cys	Lys	Asn	Arg	Arg	Cys	Gly	Gly	Glu	Leu	Gly	Asp	
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Phe	Thr	Gly	Tyr	Ile	Glu	Ser	Pro	Asn	Tyr	Pro	Gly	Asn	Tyr	Pro	Ala	
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Tyr	Glu	Thr	Cys	Gln	Thr	Tyr	Glu	Arg	Pro	Ile	Ala	Phe	Thr	Ser	Arg	
		275					280					285				
Ser	Lys	Lys	Leu	Trp	Ile	Gln	Phe	Lys	Ser	Asn	Glu	Gly	Asn	Ser	Ala	
	290					295					300					

Arg Gly Phe Gln Val Pro Tyr Val Thr Tyr Asp Glu Asp Tyr Gln Glu
 305 310 315 320
 Leu Ile Glu Asp Ile Val Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn
 325 330 335
 His Gln Glu Ile Leu Lys Asp Lys Lys Leu Ile Lys Ala Leu Phe Asp
 340 345 350
 Val Leu Ala His Pro Gln Asn Tyr Phe Lys Tyr Thr Ala Gln Glu Ser
 355 360 365
 Arg Glu Met Phe Pro Arg Ser Phe Ile Arg Leu Leu Arg Ser Lys Val
 370 375 380
 Ser Arg Phe Leu Arg Pro Tyr Lys
 385 390

<210> 40
 <211> 162
 <212> PRT
 <213> Mouse

<400> 40
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 Gln Phe Lys Ser Asn Glu Gly Asn Ser Ala Arg Gly Phe Gln Val Pro
 65 70 75 80
 Tyr Val Thr Tyr Asp Glu Asp Tyr Gln Glu Leu Ile Glu Asp Ile Val
 85 90 95
 Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn His Gln Glu Ile Leu Lys
 100 105 110
 Asp Lys Lys Leu Ile Lys Ala Leu Phe Asp Val Leu Ala His Pro Gln
 115 120 125
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 <212> DNA
 <213> Homo sapiens

<400> 41
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 <211> 1041
 <212> DNA
 <213> Homo sapiens

<400> 42

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<210> 43

<211> 346

<212> PRT

<213> Homo sapiens

<400> 43

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      20             25             30
Arg His Met Pro Trp Asn Ile Thr Arg Met Pro Asn His Leu His His
      35             40             45
Ser Thr Gln Glu Asn Ala Ile Leu Ala Ile Glu Gln Tyr Glu Glu Leu
      50             55             60
Val Asp Val Asn Cys Ser Ala Val Leu Arg Phe Phe Phe Cys Ala Met
      65             70             75             80
Tyr Ala Pro Ile Cys Thr Leu Glu Phe Leu His Asp Pro Ile Lys Pro
      85             90             95
Cys Lys Ser Val Cys Gln Arg Ala Arg Asp Asp Cys Glu Pro Leu Met
      100            105            110
Lys Met Tyr Asn His Ser Trp Pro Glu Ser Leu Ala Cys Asp Glu Leu
      115            120            125
Pro Val Tyr Asp Arg Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr
      130            135            140
Asp Leu Pro Glu Asp Val Lys Trp Ile Asp Ile Thr Pro Asp Met Met
      145            150            155            160
Val Gln Glu Arg Pro Leu Asp Val Asp Cys Lys Arg Leu Ser Pro Asp
      165            170            175
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Arg Cys Lys Cys Lys Lys Val Lys Pro Thr Leu Ala Thr Tyr Leu Ser
 180 185 190
 Lys Asn Tyr Ser Tyr Val Ile His Ala Lys Ile Lys Ala Val Gln Arg
 195 200 205
 Ser Gly Cys Asn Glu Val Thr Thr Val Val Asp Val Lys Glu Ile Phe
 210 215 220
 Lys Ser Ser Ser Pro Ile Pro Arg Thr Gln Val Pro Leu Ile Thr Asn
 225 230 235 240
 Ser Ser Cys Gln Cys Pro His Ile Leu Pro His Gln Asp Val Leu Ile
 245 250 255
 Met Cys Tyr Glu Trp Arg Ser Arg Met Met Leu Leu Glu Asn Cys Leu
 260 265 270
 Val Glu Lys Trp Arg Asp Gln Leu Ser Lys Arg Ser Ile Gln Trp Glu
 275 280 285
 Glu Arg Leu Gln Glu Gln Arg Arg Thr Val Gln Asp Lys Lys Lys Thr
 290 295 300
 Ala Gly Arg Thr Ser Arg Ser Asn Pro Pro Lys Pro Lys Gly Lys Pro
 305 310 315 320
 Pro Ala Pro Lys Pro Ala Ser Pro Lys Lys Asn Ile Lys Thr Arg Ser
 325 330 335
 Ala Gln Lys Arg Thr Asn Pro Lys Arg Val
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 <211> 749
 <212> DNA
 <213> Homo sapiens

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 cagtcagagc tataagagat gatagaaaaa agccttcact tcaaagaagt caaatttcat 600
 gaagaaaacc tctggcacat tgacaaatac taaatgtgca agtatataga ttttgtaata 660
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<210> 45
 <211> 501
 <212> DNA
 <213> Homo sapiens

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<210> 46
<211> 166
<212> PRT
<213> Homo sapiens

<400> 46
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Thr Leu Ser Arg Gly Trp Gly Asp Asp Ile Thr Trp Val Gln Thr Tyr
35 40 45
Glu Glu Gly Leu Phe Tyr Ala Gln Lys Ser Lys Lys Pro Leu Met Val
50 55 60
Ile His His Leu Glu Asp Cys Gln Tyr Ser Gln Ala Leu Lys Lys Val
65 70 75 80
Phe Ala Gln Asn Glu Glu Ile Gln Glu Met Ala Gln Asn Lys Phe Ile
85 90 95
Met Leu Asn Leu Met His Glu Thr Thr Asp Lys Asn Leu Ser Pro Asp
100 105 110
Gly Gln Tyr Val Pro Arg Ile Met Phe Val Asp Pro Ser Leu Thr Val
115 120 125
Arg Ala Asp Ile Ala Gly Arg Tyr Ser Asn Arg Leu Tyr Thr Tyr Glu
130 135 140
Pro Arg Asp Leu Pro Leu Leu Ile Glu Asn Met Lys Lys Ala Leu Arg
145 150 155 160
Leu Ile Gln Ser Glu Leu
165

<210> 47
<211> 3493
<212> DNA
<213> Homo sapiens

<400> 47
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<210> 48
 <211> 925
 <212> PRT
 <213> Homo sapiens

<400> 48

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Arg	Ser	His	Ala	Ala	Glu	Ala	Pro	Gly	Asp	Pro	Gln	Ala	Ala	Ala	Ser	35	40	45	
Leu	Leu	Ala	Pro	Met	Asp	Val	Gly	Glu	Glu	Pro	Leu	Glu	Lys	Ala	Ala	50	55	60	
Arg	Ala	Arg	Thr	Ala	Lys	Asp	Pro	Asn	Thr	Tyr	Lys	Val	Leu	Ser	Leu	65	70	75	80
Val	Leu	Ser	Val	Cys	Val	Leu	Thr	Thr	Ile	Leu	Gly	Cys	Ile	Phe	Gly	85	90	95	
Leu	Lys	Pro	Ser	Cys	Ala	Lys	Glu	Val	Lys	Ser	Cys	Lys	Gly	Arg	Cys	100	105	110	
Phe	Glu	Arg	Thr	Phe	Gly	Asn	Cys	Arg	Cys	Asp	Ala	Ala	Cys	Val	Glu	115	120	125	
Leu	Gly	Asn	Cys	Cys	Leu	Asp	Tyr	Gln	Glu	Thr	Cys	Ile	Glu	Pro	Glu	130	135	140	
His	Ile	Trp	Thr	Cys	Asn	Lys	Phe	Arg	Cys	Gly	Glu	Lys	Arg	Leu	Thr	145	150	155	160
Arg	Ser	Leu	Cys	Ala	Cys	Ser	Asp	Asp	Cys	Lys	Asp	Lys	Gly	Asp	Cys	165	170	175	
Cys	Ile	Asn	Tyr	Ser	Ser	Val	Cys	Gln	Gly	Glu	Lys	Ser	Trp	Val	Glu	180	185	190	
Glu	Pro	Cys	Glu	Ser	Ile	Asn	Glu	Pro	Gln	Cys	Pro	Ala	Gly	Phe	Glu	195	200	205	
Thr	Pro	Pro	Thr	Leu	Leu	Phe	Ser	Leu	Asp	Gly	Phe	Arg	Ala	Glu	Tyr	210	215	220	
Leu	His	Thr	Trp	Gly	Gly	Leu	Leu	Pro	Val	Ile	Ser	Lys	Leu	Lys	Lys	225	230	235	240
Cys	Gly	Thr	Tyr	Thr	Lys	Asn	Met	Arg	Pro	Val	Tyr	Pro	Thr	Lys	Thr	245	250	255	
Phe	Pro	Asn	His	Tyr	Ser	Ile	Val	Thr	Gly	Leu	Tyr	Pro	Glu	Ser	His	260	265	270	
Gly	Ile	Ile	Asp	Asn	Lys	Met	Tyr	Asp	Pro	Lys	Met	Asn	Ala	Ser	Phe	275	280	285	

Ser Leu Lys Ser Lys Glu Lys Phe Asn Pro Glu Trp Tyr Lys Gly Glu
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 Pro Ile Trp Val Thr Ala Lys Tyr Gln Gly Leu Lys Ser Gly Thr Phe
 305 310 315 320
 Phe Trp Pro Gly Ser Asp Val Glu Ile Asn Gly Ile Phe Pro Asp Ile
 325 330 335
 Tyr Lys Met Tyr Asn Gly Ser Val Pro Phe Glu Glu Arg Ile Leu Ala
 340 345 350
 Val Leu Gln Trp Leu Gln Leu Pro Lys Asp Glu Arg Pro His Phe Tyr
 355 360 365
 Thr Leu Tyr Leu Glu Glu Pro Asp Ser Ser Gly His Ser Tyr Gly Pro
 370 375 380
 Val Ser Ser Glu Val Ile Lys Ala Leu Gln Arg Val Asp Gly Met Val
 385 390 395 400
 Gly Met Leu Met Asp Gly Leu Lys Glu Leu Asn Leu His Arg Cys Leu
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 Asn Leu Ile Leu Ile Ser Asp His Gly Met Glu Gln Gly Ser Cys Lys
 420 425 430
 Lys Tyr Ile Tyr Leu Asn Lys Tyr Leu Gly Asp Val Lys Asn Ile Lys
 435 440 445
 Val Ile Tyr Gly Pro Ala Ala Arg Leu Arg Pro Ser Asp Val Pro Asp
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 Lys Tyr Tyr Ser Phe Asn Tyr Glu Gly Ile Ala Arg Asn Leu Ser Cys
 465 470 475 480
 Arg Glu Pro Asn Gln His Phe Lys Pro Tyr Leu Lys His Phe Leu Pro
 485 490 495
 Lys Arg Leu His Phe Ala Lys Ser Asp Arg Ile Glu Pro Leu Thr Phe
 500 505 510
 Tyr Leu Asp Pro Gln Trp Gln Leu Ala Leu Asn Pro Ser Glu Arg Lys
 515 520 525
 Tyr Cys Gly Ser Gly Phe His Gly Ser Asp Asn Val Phe Ser Asn Met
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 545 550 555 560
 Ala Asp Thr Phe Glu Asn Ile Glu Val Tyr Asn Leu Met Cys Asp Leu
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 Leu Asn Leu Thr Pro Ala Pro Asn Asn Gly Thr His Gly Ser Leu Asn
 580 585 590
 His Leu Leu Lys Asn Pro Val Tyr Thr Pro Lys His Pro Lys Glu Val
 595 600 605

His Pro Leu Val Gln Cys Pro Phe Thr Arg Asn Pro Arg Asp Asn Leu
 610 615 620
 Gly Cys Ser Cys Asn Pro Ser Ile Leu Pro Ile Glu Asp Phe Gln Thr
 625 630 635 640
 Gln Phe Asn Leu Thr Val Ala Glu Glu Lys Ile Ile Lys His Glu Thr
 645 650 655
 Leu Pro Tyr Gly Arg Pro Arg Val Leu Gln Lys Glu Asn Thr Ile Cys
 660 665 670
 Leu Leu Ser Gln His Gln Phe Met Ser Gly Tyr Ser Gln Asp Ile Leu
 675 680 685
 Met Pro Leu Trp Thr Ser Tyr Thr Val Asp Arg Asn Asp Ser Phe Ser
 690 695 700
 Thr Glu Asp Phe Ser Asn Cys Leu Tyr Gln Asp Phe Arg Ile Pro Leu
 705 710 715 720
 Ser Pro Val His Lys Cys Ser Phe Tyr Lys Asn Asn Thr Lys Val Ser
 725 730 735
 Tyr Gly Phe Leu Ser Pro Pro Gln Leu Asn Lys Asn Ser Ser Gly Ile
 740 745 750
 Tyr Ser Glu Ala Leu Leu Thr Thr Asn Ile Val Pro Met Tyr Gln Ser
 755 760 765
 Phe Gln Val Ile Trp Arg Tyr Phe His Asp Thr Leu Leu Arg Lys Tyr
 770 775 780
 Ala Glu Glu Arg Asn Gly Val Asn Val Val Ser Gly Pro Val Phe Asp
 785 790 795 800
 Phe Asp Tyr Asp Gly Arg Cys Asp Ser Leu Glu Asn Leu Arg Gln Lys
 805 810 815
 Arg Arg Val Ile Arg Asn Gln Glu Ile Leu Ile Pro Thr His Phe Phe
 820 825 830
 Ile Val Leu Thr Ser Cys Lys Asp Thr Ser Gln Thr Pro Leu His Cys
 835 840 845
 Glu Asn Leu Asp Thr Leu Ala Phe Ile Leu Pro His Arg Thr Asp Asn
 850 855 860
 Ser Glu Ser Cys Val His Gly Lys His Asp Ser Ser Trp Val Glu Glu
 865 870 875 880
 Leu Leu Met Leu His Arg Ala Arg Ile Thr Asp Val Glu His Ile Thr
 885 890 895
 Gly Leu Ser Phe Tyr Gln Gln Arg Lys Glu Pro Val Ser Asp Ile Leu
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 Lys Leu Lys Thr His Leu Pro Thr Phe Ser Gln Glu Asp
 915 920 925

<210> 49
 <211> 2709
 <212> DNA
 <213> Homo sapiens

<400> 49
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 tgctctgtca tatatttact aattgtatgg ctgggaccaa aatacatgag gaataaacag 180
 ccattctctt gccgggggat tttagtgggt tataaccttg gactcacact gctgtctctg 240
 tatatgttct gtgagttagt aacaggagta tgggaaggca aatacaactt cttctgtcag 300
 ggcacacgca ccgcaggaga atcagatatg aagattatcc gtgtcctctg gtggtactac 360
 ttctccaaac tcatagaatt tatggacact ttcttcttca tcctgcgcaa gaacaaccac 420
 cagatcacgg tcctgcacgt ctaccacatg gcctcgatgc tgaacatctg gtggtttgtg 480
 atgaactggg tccccctggg ccactcttat tttggtgcc aacttaatag cttcatccac 540
 gtcctcatgt actcttacta tggtttgtcg tcagtcctt ccattgcgtcc atacctctgg 600
 tggagaagt acatcactca ggggcagctg cttcagtttg tgctgacaat catccagacc 660
 agctgcgggg tcatctggcc gtgcacattc cctcttggtt ggttgtatct ccagattgga 720
 tacatgattt ccctgattgc tctcttcaca aacttctaca ttcagacctt caacaagaaa 780
 ggggcctccc gaaggaaaga ccacctgaag gaccaccaga atgggtccat ggctgctgtg 840
 aatggacaca ccaacagctt ttcacccctg gaaaacaatg tgaagccaag gaagctgagg 900
 aaggattgaa gtcaagaagt tgaaaccctc caaaccacgt catctgattg taagcacaat 960
 atgagttgtg ccccaatgct cgtaaacagc tgctgtaact agtctggcct acaatagtgt 1020
 gattcatgta ggacttcttt catcaattca aaaccctag aaaacgtata cagattatat 1080
 aagtagggat aagatttcta acatttctgg gctctctgac ccctgcgcta gactgtgga 1140
 agggagtatt attatagtat acaacactgc tgttgccctt ttagttataa catgatagg 1200
 gctgaattgt gattcacaat ttaaaaacac tgtaatccaa actttttttt ttaactgtag 1260
 atcatgcatg tgattgtaaa tgtaaaattt tacaatggtt ttatggtaga gaaacacaca 1320
 tgccttaaaa tttaaaaagc agggcccaaa gcttattagt ttaattagg gtatgtttca 1380
 agtttgatatt aatttgtaat agctctgttt agaaaaaatc aaagaccatg atttatgaaa 1440
 ctaatgtgac ataatttcca gtgacttggt gatgtgaaat cagacacggc accttcagtt 1500
 ttgtactatt ggctttgaat caagcaggct caaatctagt ggaacagtca gtttaacttt 1560
 ttaacagatc ttattttttt attttgagt ccactattaa tgtaaaaagg ggggggctct 1620
 acagcagtcg tgatgaaact taaatatata ttctttgtcc tcgagatttt aggaagggtg 1680
 tagggtagt aggccatttt taatttctga agtgctaagt gtttttatac agcaaacaaa 1740
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 taaatttgga ttgatttatg cactgttatc tgttttgaca cagatttcct tgtaaaatgt 1920
 gcctagttaa ccaaaattaa caaagggggg gaaaggacct tagaactttt taaggtaaaa 1980
 tcaaatatag ctacagcata agagaatcga gaaatttgat agaggtaact tgtttaatgt 2040
 aaatctaata gtacttgtaa tttctttctg cttagaatct aaagatgtgt ttagaacctc 2100
 ttgtttaaaa ataatagact gcttatcata aaatcacatc tcacacattt gaggcagtgg 2160
 tcaaacaggt aaagcctatg atgtgtgtca ttttaaagtg tcggaattta gcctctgaat 2220
 accttctcca ttgggggaaa gatattcttg gaaccactca tgacatatct tagaagggtc 2280
 ttgacaatgt ataaactaat tgttggtttg atatttatgt aaatatcagt ttaccatgct 2340
 ttaattttgc acattcgtac tatagggagc ctattggttc tctattagtc ttgtgggttt 2400
 tctgtttgaa aaggagtcac ggcactctgt tacattttacc ttatcaaacc tagaatgtgt 2460
 atatttataa atgtatgtct tcattgctag gtactaattt gcagatgtct ttacatattt 2520
 caatacagaa actataacat tcaatagtgt gctgtcaaag tgtgcttagc tcacctggat 2580
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2700
 aaaaaaaaaa

<210> 50
 <211> 299
 <212> PRT
 <213> Homo sapiens

<400> 50

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Gly	Pro	Arg	Asp	Thr	Arg	Val	Lys	Gly	Trp	Phe	Leu	Leu	Asp	Asn	Tyr	
			20					25					30			
Ile	Pro	Thr	Phe	Ile	Cys	Ser	Val	Ile	Tyr	Leu	Leu	Ile	Val	Trp	Leu	
		35					40					45				
Gly	Pro	Lys	Tyr	Met	Arg	Asn	Lys	Gln	Pro	Phe	Ser	Cys	Arg	Gly	Ile	
	50					55					60					
Leu	Val	Val	Tyr	Asn	Leu	Gly	Leu	Thr	Leu	Leu	Ser	Leu	Tyr	Met	Phe	
65					70				75						80	
Cys	Glu	Leu	Val	Thr	Gly	Val	Trp	Glu	Gly	Lys	Tyr	Asn	Phe	Phe	Cys	
				85					90					95		
Gln	Gly	Thr	Arg	Thr	Ala	Gly	Glu	Ser	Asp	Met	Lys	Ile	Ile	Arg	Val	
			100					105					110			
Leu	Trp	Trp	Tyr	Tyr	Phe	Ser	Lys	Leu	Ile	Glu	Phe	Met	Asp	Thr	Phe	
			115				120					125				
Phe	Phe	Ile	Leu	Arg	Lys	Asn	Asn	His	Gln	Ile	Thr	Val	Leu	His	Val	
	130					135					140					
Tyr	His	His	Ala	Ser	Met	Leu	Asn	Ile	Trp	Trp	Phe	Val	Met	Asn	Trp	
145					150					155					160	
Val	Pro	Cys	Gly	His	Ser	Tyr	Phe	Gly	Ala	Thr	Leu	Asn	Ser	Phe	Ile	
				165					170						175	
His	Val	Leu	Met	Tyr	Ser	Tyr	Tyr	Gly	Leu	Ser	Ser	Val	Pro	Ser	Met	
			180					185					190			
Arg	Pro	Tyr	Leu	Trp	Trp	Lys	Lys	Tyr	Ile	Thr	Gln	Gly	Gln	Leu	Leu	
		195					200					205				
Gln	Phe	Val	Leu	Thr	Ile	Ile	Gln	Thr	Ser	Cys	Gly	Val	Ile	Trp	Pro	
	210					215					220					
Cys	Thr	Phe	Pro	Leu	Gly	Trp	Leu	Tyr	Phe	Gln	Ile	Gly	Tyr	Met	Ile	
225					230					235					240	
Ser	Leu	Ile	Ala	Leu	Phe	Thr	Asn	Phe	Tyr	Ile	Gln	Thr	Tyr	Asn	Lys	
				245				250						255		
Lys	Gly	Ala	Ser	Arg	Arg	Lys	Asp	His	Leu	Lys	Asp	His	Gln	Asn	Gly	
			260					265					270			
Ser	Met	Ala	Ala	Val	Asn	Gly	His	Thr	Asn	Ser	Phe	Ser	Pro	Leu	Glu	
		275					280					285				
Asn	Asn	Val	Lys	Pro	Arg	Lys	Leu	Arg	Lys	Asp						
	290					295										

<210> 51

<211> 1019
 <212> DNA
 <213> Homo sapiens

<400> 51
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 ctccctttcca tcctgcggtg acagctaaga cctcagtttt caatagcatc tagagcagtg 180
 ggactcagct ggggtgattt cgcctcccat ctccggggga atgtctgaag acaatttttg 240
 ttacctcaat gaggagtgagg aggaggatac agtgctacta ccaactagt gataaaggcc 300
 agggatgctg ctcaacctcc taccatgtac aggacgtctc cccattacaa ctaccaatc 360
 cgaagtgtca actgtgtcag gactaagaaa ccctggtttt gagtagaaaa gggcctggaa 420
 agaggggagc caacaaatct gtctgcttcc tcacattagt cattggcaaa taagcattct 480
 gtctcttttg ctgctgcctc agcacagaga gccagaactc tatcgggcac caggataaca 540
 tctctcagtg aacagagttg acaaggccta tgggaaatgc ctgatgggat tatcttcagc 600
 ttgttgagct tctaagtttc tttcccttca ttctaccctg caagccaagt tctgtaagag 660
 aaatgcctga gttctagctc aggtttttctt actctgaatt tagatctcca gacccttcct 720
 ggccacaatt caaattaagg caacaaacat ataccttcca tgaagcacac acagactttt 780
 gaaagcaagg acaatgactg cttgaattga ggccttgagg aatgaagctt tgaaggaaaa 840
 gaatactttg tttccagccc ccttcccaca ctcttcattg gttaaccact gccttcctgg 900
 accttgagc cagcgtgact gtattacatg ttgttataga aaactgattt tagagttctg 960
 atcgttcaag agaatgatta aatatacatt tcctacamaa aaaaaaaaaa aagtcgacg 1019

<210> 52
 <211> 1332
 <212> DNA
 <213> Homo sapiens

<400> 52
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 ctttgccctc ggcctcccaa agtgcagtag ccaccatgcc tggcctgttt agttttgttt 120
 caagttgaaa tacctttctt gtgttttcta attagaaaag taatatctac tcattgtaaa 180
 aactcaaaca gtgcagaaat gtagaaagta gaaagtgtaa gtccctgggt gtcccttctg 240
 cctgagcaca accactgctc acagtttgat gtatatcctt ccagagactc tcaaatttaa 300
 gcaataaatt tttattacca tgtcttttta tttgaagacg tacatttgcc tccaaagttc 360
 aacacaagtt caactgacca tatccttcca tgacctgaat agatgctatc ctttatcacg 420
 atgttcaatt gcctttgaaa gagagtagtc caggatatatt cctgatcaaa atttggcatt 480
 tttgatgata ctactctaca cagatcagac tcattgtgcag aatcgtgcct ggagagagag 540
 gtttggttaa gacagagatt tctggaaaca ttcaaattgc aaatggaaac ttgaaacca 600
 caatctaatt aggaatgtac tggaaaaata atctgaagag ttgacaaatt gtgtactaga 660
 ttgaacacat ggaatgcaat gccaatgaga ctttctgcac taaaacttat cctcatatgt 720
 acaacaatga tgtgtgtatt atataacagt gatgtgtaca tttctgacac ccatacata 780
 atatacacag tttgtataaa tgcatacatt taaaaatata tatgtacaat acagctaaca 840
 taaaactgta gtacgcctga aggatattac tagtgcctaa tattgagtat gagtcaactg 900
 gtgttcgcat caacttgga gtgcagtaat tgttataaaa ttaatcagtg cagccaacat 960
 tatttatgaa tcacatcttt gaaactgtgc agtagcatat acatatatat ttttaaataa 1020
 cttttttcac agttttccag agttactgtt gaaatctgca tcaccaaaaa aaaaaaaaaa 1080
 caagattttt ttaacaatgt agacactctt cagaccaggt aatctgcgtg tgatttccta 1140
 tttgtagatt cccaagagac ttagcagtc accagcctta atgcatgtac aggatattat 1200
 tgtgacttaa tttatctgca gtttttaatc catgtgaaat tgggaatttt taaccgaact 1260
 tggattaacc atgcctgcct ttctaagggt gcaaagtgtta cattaaatga tttatgttgt 1320
 aaaaaaaaaa aa 1332

<210> 53
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (3)
 <223> "Xaa" at position 3 can be any amino acid

<220>
 <223> Description of Artificial Sequence: Ctyokine
 receptor exctracellular motif found in many
 species.

<400> 53
 Trp Ser Xaa Trp Ser
 1 5

<210> 54
 <211> 2744
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (138)..(2387)

<400> 54
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 gcggagacga aggcgca atg gcg agg aag tta tct gta atc ttg atc ctg 170
 Met Ala Arg Lys Leu Ser Val Ile Leu Ile Leu
 1 5 10
 acc ttt gcc ctc tct gtc aca aat ccc ctt cat gaa cta aaa gca gct 218
 Thr Phe Ala Leu Ser Val Thr Asn Pro Leu His Glu Leu Lys Ala Ala
 15 20 25
 gct ttc ccc cag acc act gag aaa att agt ccg aat tgg gaa tct ggc 266
 Ala Phe Pro Gln Thr Thr Glu Lys Ile Ser Pro Asn Trp Glu Ser Gly
 30 35 40
 att aat gtt gac ttg gca att tcc aca cgg caa tat cat cta caa cag 314
 Ile Asn Val Asp Leu Ala Ile Ser Thr Arg Gln Tyr His Leu Gln Gln
 45 50 55
 ctt ttc tac cgc tat gga gaa aat aat tct ttg tca gtt gaa ggg ttc 362
 Leu Phe Tyr Arg Tyr Gly Glu Asn Asn Ser Leu Ser Val Glu Gly Phe
 60 65 70 75
 aga aaa tta ctt caa aat ata ggc ata gat aag att aaa aga atc cat 410
 Arg Lys Leu Leu Gln Asn Ile Gly Ile Asp Lys Ile Lys Arg Ile His
 80 85 90
 ata cac cat gac cac gac cat cac tca gac cac gag cat cac tca gac 458
 Ile His His Asp His Asp His His Ser Asp His Glu His His Ser Asp
 95 100 105
 cat gag cgt cac tca gac cat gag cat cac tca gac cac gag cat cac 506
 His Glu Arg His Ser Asp His Glu His His Ser Asp His Glu His His
 110 115 120

tct gac cat aat cat gct gct tct ggt aaa aat aag cga aaa gct ctt	554
Ser Asp His Asn His Ala Ala Ser Gly Lys Asn Lys Arg Lys Ala Leu	
125 130 135	
tgc cca gac cat gac tca gat agt tca ggt aaa gat cct aga aac agc	602
Cys Pro Asp His Asp Ser Asp Ser Ser Gly Lys Asp Pro Arg Asn Ser	
140 145 150 155	
cag ggg aaa gga gct cac cga cca gaa cat gcc agt ggt aga agg aat	650
Gln Gly Lys Gly Ala His Arg Pro Glu His Ala Ser Gly Arg Arg Asn	
160 165 170	
gtc aag gac agt gtt agt gct agt gaa gtg acc tca act gtg tac aac	698
Val Lys Asp Ser Val Ser Ala Ser Glu Val Thr Ser Thr Val Tyr Asn	
175 180 185	
act gtc tct gaa gga act cac ttt cta gag aca ata gag act cca aga	746
Thr Val Ser Glu Gly Thr His Phe Leu Glu Thr Ile Glu Thr Pro Arg	
190 195 200	
cct gga aaa ctc ttc ccc aaa gat gta agc agc tcc act cca ccc agt	794
Pro Gly Lys Leu Phe Pro Lys Asp Val Ser Ser Ser Thr Pro Pro Ser	
205 210 215	
gtc aca tca aag agc cgg gtg agc cgg ctg gct ggt agg aaa aca aat	842
Val Thr Ser Lys Ser Arg Val Ser Arg Leu Ala Gly Arg Lys Thr Asn	
220 225 230 235	
gaa tct gtg agt gag ccc cga aaa ggc ttt atg tat tcc aga aac aca	890
Glu Ser Val Ser Glu Pro Arg Lys Gly Phe Met Tyr Ser Arg Asn Thr	
240 245 250	
aat gaa aat cct cag gag tgt ttc aat gca tca aag cta ctg aca tct	938
Asn Glu Asn Pro Gln Glu Cys Phe Asn Ala Ser Lys Leu Leu Thr Ser	
255 260 265	
cat ggc atg ggc atc cag gtt ccg ctg aat gca aca gag ttc aac tat	986
His Gly Met Gly Ile Gln Val Pro Leu Asn Ala Thr Glu Phe Asn Tyr	
270 275 280	
ctc tgt cca gcc atc atc aac caa att gat gct aga tct tgt ctg att	1034
Leu Cys Pro Ala Ile Ile Asn Gln Ile Asp Ala Arg Ser Cys Leu Ile	
285 290 295	
cat aca agt gaa aag aag gct gaa atc cct cca aag acc tat tca tta	1082
His Thr Ser Glu Lys Lys Ala Glu Ile Pro Pro Lys Thr Tyr Ser Leu	
300 305 310 315	
caa ata gcc tgg gtt ggt ggt ttt ata gcc att tcc atc atc agt ttc	1130
Gln Ile Ala Trp Val Gly Gly Phe Ile Ala Ile Ser Ile Ile Ser Phe	
320 325 330	
ctg tct ctg ctg ggg gtt atc tta gtg cct ctc atg aat cgg gtg ttt	1178
Leu Ser Leu Leu Gly Val Ile Leu Val Pro Leu Met Asn Arg Val Phe	
335 340 345	
ttc aaa ttt ctc ctg agt ttc ctt gtg gca ctg gcc gtt ggg act ttg	1226
Phe Lys Phe Leu Leu Ser Phe Leu Val Ala Leu Ala Val Gly Thr Leu	
350 355 360	

agt ggt gat gct ttt tta cac ctt ctt cca cat tct cat gca agt cac	1274
Ser Gly Asp Ala Phe Leu His Leu Leu Pro His Ser His Ala Ser His	
365 370 375	
cac cat agt cat agc cat gaa gaa cca gca atg gaa atg aaa aga gga	1322
His His Ser His Ser His Glu Glu Pro Ala Met Glu Met Lys Arg Gly	
380 385 390 395	
cca ctt ttc agt cat ctg tct tct caa aac ata gaa gaa agt gcc tat	1370
Pro Leu Phe Ser His Leu Ser Ser Gln Asn Ile Glu Glu Ser Ala Tyr	
400 405 410	
ttt gat tcc acg tgg aag ggt cta aca gct cta gga ggc ctg tat ttc	1418
Phe Asp Ser Thr Trp Lys Gly Leu Thr Ala Leu Gly Gly Leu Tyr Phe	
415 420 425	
atg ttt ctt gtt gaa cat gtc ctc aca ttg atc aaa caa ttt aaa gat	1466
Met Phe Leu Val Glu His Val Leu Thr Leu Ile Lys Gln Phe Lys Asp	
430 435 440	
aag aag aaa aag aat cag aag aaa cct gaa aat gat gat gat gtg gag	1514
Lys Lys Lys Lys Asn Gln Lys Lys Pro Glu Asn Asp Asp Asp Val Glu	
445 450 455	
att aag aag cag ttg tcc aag tat gaa tct caa ctt tca aca aat gag	1562
Ile Lys Lys Gln Leu Ser Lys Tyr Glu Ser Gln Leu Ser Thr Asn Glu	
460 465 470 475	
gag aaa gta gat aca gat gat cga act gaa ggc tat tta cga gca gac	1610
Glu Lys Val Asp Thr Asp Asp Arg Thr Glu Gly Tyr Leu Arg Ala Asp	
480 485 490	
tca caa gag ccc tcc cac ttt gat tct cag cag cct gca gtc ttg gaa	1658
Ser Gln Glu Pro Ser His Phe Asp Ser Gln Gln Pro Ala Val Leu Glu	
495 500 505	
gaa gaa gag gtc atg ata gct cat gct cat cca cag gaa gtc tac aat	1706
Glu Glu Glu Val Met Ile Ala His Ala His Pro Gln Glu Val Tyr Asn	
510 515 520	
gaa tat gta ccc aga ggg tgc aag aat aaa tgc cat tca cat ttc cac	1754
Glu Tyr Val Pro Arg Gly Cys Lys Asn Lys Cys His Ser His Phe His	
525 530 535	
gat aca ctc ggc cag tca gac gat ctc att cac cac cat cat gac tac	1802
Asp Thr Leu Gly Gln Ser Asp Asp Leu Ile His His His His Asp Tyr	
540 545 550 555	
cat cat att ctc cat cat cac cac cac caa aac cac cat cct cac agt	1850
His His Ile Leu His His His His His Gln Asn His His Pro His Ser	
560 565 570	
cac agc cag cgc tac tct cgg gag gag ctg aaa gat gcc ggc gtc gcc	1898
His Ser Gln Arg Tyr Ser Arg Glu Glu Leu Lys Asp Ala Gly Val Ala	
575 580 585	
act ttg gcc tgg atg gtg ata atg ggt gat ggc ctg cac aat ttc agc	1946
Thr Leu Ala Trp Met Val Ile Met Gly Asp Gly Leu His Asn Phe Ser	
590 595 600	

gat ggc cta gca att ggt gct gct ttt act gaa ggc tta tca agt ggt	1994
Asp Gly Leu Ala Ile Gly Ala Ala Phe Thr Glu Gly Leu Ser Ser Gly	
605 610 615	
tta agt act tct gtt gct gtg ttc tgt cat gag ttg cct cat gaa tta	2042
Leu Ser Thr Ser Val Ala Val Phe Cys His Glu Leu Pro His Glu Leu	
620 625 630 635	
ggg gac ttt gct gtt cta cta aag gct ggc atg acc gtt aag cag gct	2090
Gly Asp Phe Ala Val Leu Leu Lys Ala Gly Met Thr Val Lys Gln Ala	
640 645 650	
gtc ctt tat aat gca ttg tca gcc atg ctg gcg tat ctt gga atg gca	2138
Val Leu Tyr Asn Ala Leu Ser Ala Met Leu Ala Tyr Leu Gly Met Ala	
655 660 665	
aca gga att ttc att ggt cat tat gct gaa aat gtt tct atg tgg ata	2186
Thr Gly Ile Phe Ile Gly His Tyr Ala Glu Asn Val Ser Met Trp Ile	
670 675 680	
ttt gca ctt act gct ggc tta ttc atg tat gtt gct ctg gtt gat atg	2234
Phe Ala Leu Thr Ala Gly Leu Phe Met Tyr Val Ala Leu Val Asp Met	
685 690 695	
gta cct gaa atg ctg cac aat gat gct agt gac cat gga tgt agc cgc	2282
Val Pro Glu Met Leu His Asn Asp Ala Ser Asp His Gly Cys Ser Arg	
700 705 710 715	
tgg ggg tat ttc ttt tta cag aat gct ggg atg ctt ttg ggt ttt gga	2330
Trp Gly Tyr Phe Phe Leu Gln Asn Ala Gly Met Leu Leu Gly Phe Gly	
720 725 730	
att atg tta ctt att tcc ata ttt gaa cat aaa atc gtg ttt cgt ata	2378
Ile Met Leu Leu Ile Ser Ile Phe Glu His Lys Ile Val Phe Arg Ile	
735 740 745	
aat ttc tag ttaaggttta aatgctagag tagcttaaaa agttgtcata	2427
Asn Phe	

gtttcagtag gtcataaggga gatgagtttg tatgctgtac tatgcagcgt ttaaagttag	2487
tggtgtttgt gatttttgta ttgaatattg ctgtctgtta caaagtcagt taaaggtacg	2547
ttttaatatt taagttattc tatcttgag ataaaatctg tatgtgcaat tcaccggtat	2607
taccagttta ttatgtaaac aagagatttg gcatgacatg ttctgtatgt ttcaggga	2667
aatgtcttta atgctttttc aagaactaac acagttattc ctatactgga ttttaggtct	2727
ctgaagaact gctggtg	2744

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<400> 55

000

<210> 56
<211> 293
<212> DNA
<213> Homo sapiens

<220>
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<222> (190)
<223> "n" at position 190 can be any base

<400> 56
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acgaccacca acatgaatca gttttaggc atttacaagc cacagctgaa aataaaaaatc 120
tgtctgtgtt gaatagggcat ttaacaaatt acttgaaaac tgcaagaatc ataattatta 180
taaatttaan gtttgtgatt caaacatggg taagatcaca gtcattggga gaagcccaac 240
agattcctgt gatgatcctt attttcttcc tatatcttta tatacatagg agg 293

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<211> 2053
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<213> Homo sapiens

<220>
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<400> 57
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agctccgggg aaacgcgagc cgcg atg cct ggg ggg tgc tcc cg ggc ccc 111
Met Pro Gly Gly Cys Ser Arg Gly Pro
1 5
gcc gcc ggg gac ggg cgt ctg cgg ctg gcg cga cta gcg ctg gta ctc 159
Ala Ala Gly Asp Gly Arg Leu Arg Leu Ala Arg Leu Ala Leu Val Leu
10 15 20 25
ctg ggc tgg gtc tcc tcg tct tct ccc acc tcc tcg gca tcc tcc ttc 207
Leu Gly Trp Val Ser Ser Ser Ser Pro Thr Ser Ser Ala Ser Ser Phe
30 35 40
tcc tcc tcg gcg ccg ttc ctg gct tcc gcc gtg tcc gcc cag ccc ccg 255
Ser Ser Ser Ala Pro Phe Leu Ala Ser Ala Val Ser Ala Gln Pro Pro
45 50 55
ctg ccg gac cag tgc ccc gcg ctg tgc gag tgc tcc gag gca gcg cgc 303
Leu Pro Asp Gln Cys Pro Ala Leu Cys Glu Cys Ser Glu Ala Ala Arg
60 65 70
aca gtc aag tgc gtt aac cgc aat ctg acc gag gtg ccc acg gac ctg 351
Thr Val Lys Cys Val Asn Arg Asn Leu Thr Glu Val Pro Thr Asp Leu
75 80 85
ccc gcc tac gtg cgc aac ctc ttc ctt acc ggc aac cag ctg gcc gtg 399
Pro Ala Tyr Val Arg Asn Leu Phe Leu Thr Gly Asn Gln Leu Ala Val

90	95	100	105	
ctc cct gcc ggc gcc ttc gcc cgc cgg ccg ccg ctg gcg gag ctg gcc	447			
Leu Pro Ala Gly Ala Phe Ala Arg Arg Pro Pro Leu Ala Glu Leu Ala				
110 115 120				
gcg ctc aac ctc agc ggc agc cgc ctg gac gag gtg cgc gcg ggc gcc	495			
Ala Leu Asn Leu Ser Gly Ser Arg Leu Asp Glu Val Arg Ala Gly Ala				
125 130 135				
ttc gag cat ctg ccc agc ctg cgc cag ctc gac ctc agc cac aac cca	543			
Phe Glu His Leu Pro Ser Leu Arg Gln Leu Asp Leu Ser His Asn Pro				
140 145 150				
ctg gcc gac ctc agt ccc ttc gct ttc tcg ggc agc aat gcc agc gtc	591			
Leu Ala Asp Leu Ser Pro Phe Ala Phe Ser Gly Ser Asn Ala Ser Val				
155 160 165				
tcg gcc ccc agt ccc ctt gtg gaa ctg atc ctg aac cac atc gtg ccc	639			
Ser Ala Pro Ser Pro Leu Val Glu Leu Ile Leu Asn His Ile Val Pro				
170 175 180 185				
cct gaa gat gag cgg cag aac cgg agc ttc gag ggc atg gtg gtg gcg	687			
Pro Glu Asp Glu Arg Gln Asn Arg Ser Phe Glu Gly Met Val Val Ala				
190 195 200				
gcc ctg ctg gcg ggc cgt gca ctg cag ggg ctc cgc cgc ttg gag ctg	735			
Ala Leu Leu Ala Gly Arg Ala Leu Gln Gly Leu Arg Arg Leu Glu Leu				
205 210 215				
gcc agc aac cac ttc ctt tac ctg ccg cgg gat gtg ctg gcc caa ctg	783			
Ala Ser Asn His Phe Leu Tyr Leu Pro Arg Asp Val Leu Ala Gln Leu				
220 225 230				
ccc agc ctc agg cac ctg gac tta agt aat aat tcg ctg gtg agc ctg	831			
Pro Ser Leu Arg His Leu Asp Leu Ser Asn Asn Ser Leu Val Ser Leu				
235 240 245				
acc tac gtg tcc ttc cgc aac ctg aca cat cta gaa agc ctc cac ctg	879			
Thr Tyr Val Ser Phe Arg Asn Leu Thr His Leu Glu Ser Leu His Leu				
250 255 260 265				
gag gac aat gcc ctc aag gtc ctt cac aat ggc acc ctg gct gag ttg	927			
Glu Asp Asn Ala Leu Lys Val Leu His Asn Gly Thr Leu Ala Glu Leu				
270 275 280				
caa ggt cta ccc cac att agg gtt ttc ctg gac aac aat ccc tgg gtc	975			
Gln Gly Leu Pro His Ile Arg Val Phe Leu Asp Asn Asn Pro Trp Val				
285 290 295				
tgc gac tgc cac atg gca gac atg gtg acc tgg ctc aag gaa aca gag	1023			
Cys Asp Cys His Met Ala Asp Met Val Thr Trp Leu Lys Glu Thr Glu				
300 305 310				
gta gtg cag ggc aaa gac cgg ctc acc tgt gca tat ccg gaa aaa atg	1071			
Val Val Gln Gly Lys Asp Arg Leu Thr Cys Ala Tyr Pro Glu Lys Met				
315 320 325				
agg aat cgg gtc ctc ttg gaa ctc aac agt gct gac ctg gac tgt gac	1119			
Arg Asn Arg Val Leu Leu Glu Leu Asn Ser Ala Asp Leu Asp Cys Asp				

330	335	340	345	
ccg att ctt ccc cca tcc ctg caa acc tct tat gtc ttc ctg ggt att				1167
Pro Ile Leu Pro Pro Ser Leu Gln Thr Ser Tyr Val Phe Leu Gly Ile	350	355	360	
ggt tta gcc ctg ata ggc gct att ttc ctc ctg gtt ttg tat ttg aac				1215
Val Leu Ala Leu Ile Gly Ala Ile Phe Leu Leu Val Leu Tyr Leu Asn	365	370	375	
cgc aag ggg ata aaa aag tgg atg cat aac atc aga gat gcc tgc agg				1263
Arg Lys Gly Ile Lys Lys Trp Met His Asn Ile Arg Asp Ala Cys Arg	380	385	390	
gat cac atg gaa ggg tat cat tac aga tat gaa atc aat gcg gac ccc				1311
Asp His Met Glu Gly Tyr His Tyr Arg Tyr Glu Ile Asn Ala Asp Pro	395	400	405	
aga tta aca aac ctc agt tct aac tcg gat gtc tga gaaatattag				1357
Arg Leu Thr Asn Leu Ser Ser Asn Ser Asp Val	410	415	420	
aggacagacc aaggacaact ctgcatgaga tgtagactta agctttatcc ctactaggct				1417
tgctccactt tcctcctcca ctatagatac aacggacttt gactaaaagc agtgaagggg				1477
atgtgcttcc ttgttatgta aagtttctcg gtgtgttctg ttaatgtaag acgatgaaca				1537
gttgtgtata gtgttttacc ctcttctttt tcttggaact cctcaacacg tatggagggg				1597
tttttcaggt ttcagcatga acatgggctt cttgctgtct gtctctctct cagtacagtt				1657
caaggtgtag caagtgtacc cacacagata gcattcaaca aaagctgcct caactttttc				1717
gagaaaaata ctttattcat aaatatcagt tttattctca tgtacctaag ttgtggagaa				1777
aataattgca tcctataaac tgcctgcaga cgtagcagg ctcttcaaaa taactccatg				1837
gtgcacagga gcacctgcat ccaagagcat gcttacattt tactgttctg catattacaa				1897
aaaataactt gcaacttcat aacttctttg acaaagtaaa ttactttttt gattgcagtt				1957
tatatgaaaa tgtactgatt tttttttaat aaactgcac gagatccaac cgactgaatt				2017
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<213> Homo sapiens

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tttgttatgg ttcataagga cagaggttta cacaggtttt atatatgtac acactgacaa 120
tactatatca caacatcaga ggcaccattt ttgccacaga attaggtaat gaataaaaact 180
tctccaaatt aatctgttta aaaaatatct aaaatggtac agtatatttg ag 232
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<210> 60

<211> 281

<212> DNA

<213> Homo sapiens

<400> 60

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tacaaaaata tctgtattat ctataaaaat tgaactctaa tgagtcactg atacgggagg 60
cagcaatacc cgactgtgct gacatgcaga aggaagacag ctctgtccca ccaaccctat 120
agcagaacat ttgtattgag tggcacgtgg gctgagtcac ttgtaaggtc tcaaaaacct 180
ggacactttg gaacgtagca atcggatgaa cgatcttggg aacatctctc gggactcctg 240
ggctgtgtac ttgaaatagt tctgggggatg ggccaggaca t 281
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<211> 3085

<212> DNA

<213> Homo sapiens

<220>

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<222> (256)..(3012)

<400> 61

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cgcgcttgcc aggccgacgg gtctggccca gcctggcgcc aaggggttcg tgcgctgtgg 120
agacgcggag ggtcgaggcg gcgcggcctg agtgaaaccc aatggaaaaa gcatgacatt 180
tagaagtaga agacttagct tcaaatccct actccttcac ttactaattt tgtgatttgg 240
aaatatccgc gcaag atg ttg acg ttg cag act tgg gta gtg caa gcc ttg 291
          Met Leu Thr Leu Gln Thr Trp Val Val Gln Ala Leu
              1             5             10
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ttt att ttc ctc acc act gaa tct aca ggt gaa ctt cta gat cca tgt 339
Phe Ile Phe Leu Thr Thr Glu Ser Thr Gly Glu Leu Leu Asp Pro Cys
          15             20             25
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```
ggt tat atc agt cct gaa tct cca gtt gta caa ctt cat tct aat ttc 387
Gly Tyr Ile Ser Pro Glu Ser Pro Val Val Gln Leu His Ser Asn Phe
          30             35             40
```

```
act gca gtt tgt gtg cta aag gaa aaa tgt atg gat tat ttt cat gta 435
Thr Ala Val Cys Val Leu Lys Glu Lys Cys Met Asp Tyr Phe His Val
          45             50             55             60
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aat gct aat tac att gtc tgg aaa aca aac cat ttt act att cct aag 483
Asn Ala Asn Tyr Ile Val Trp Lys Thr Asn His Phe Thr Ile Pro Lys
          65             70             75
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gag caa tat act atc ata aac aga aca gca tcc agt gtc acc ttt aca	531
Glu Gln Tyr Thr Ile Ile Asn Arg Thr Ala Ser Ser Val Thr Phe Thr	
80 85 90	
gat ata gct tca tta aat att cag ctc act tgc aac att ctt aca ttc	579
Asp Ile Ala Ser Leu Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr Phe	
95 100 105	
gga cag ctt gaa cag aat gtt tat gga atc aca ata att tca ggc ttg	627
Gly Gln Leu Glu Gln Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly Leu	
110 115 120	
cct cca gaa aaa cct aaa aat ttg agt tgc att gtg aac gag ggg aag	675
Pro Pro Glu Lys Pro Lys Asn Leu Ser Cys Ile Val Asn Glu Gly Lys	
125 130 135 140	
aaa atg agg tgt gag tgg gat ggt gga agg gaa aca cac ttg gag aca	723
Lys Met Arg Cys Glu Trp Asp Gly Gly Arg Glu Thr His Leu Glu Thr	
145 150 155	
aac ttc act tta aaa tct gaa tgg gca aca cac aag ttt gct gat tgc	771
Asn Phe Thr Leu Lys Ser Glu Trp Ala Thr His Lys Phe Ala Asp Cys	
160 165 170	
aaa gca aaa cgt gac acc ccc acc tca tgc act gtt gat tat tct act	819
Lys Ala Lys Arg Asp Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser Thr	
175 180 185	
gtg tat ttt gtc aac att gaa gtc tgg gta gaa gca gag aat gcc ctt	867
Val Tyr Phe Val Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu	
190 195 200	
ggg aag gtt aca tca gat cat atc aat ttt gat cct gta tat aaa gtg	915
Gly Lys Val Thr Ser Asp His Ile Asn Phe Asp Pro Val Tyr Lys Val	
205 210 215 220	
aag ccc aat ccg cca cat aat tta tca gtg atc aac tca gag gaa ctg	963
Lys Pro Asn Pro Pro His Asn Leu Ser Val Ile Asn Ser Glu Glu Leu	
225 230 235	
tct agt atc tta aaa ttg aca tgg acc aac cca agt att aag agt gtt	1011
Ser Ser Ile Leu Lys Leu Thr Trp Thr Asn Pro Ser Ile Lys Ser Val	
240 245 250	
ata ata cta aaa tat aac att caa tat agg acc aaa gat gcc tca act	1059
Ile Ile Leu Lys Tyr Asn Ile Gln Tyr Arg Thr Lys Asp Ala Ser Thr	
255 260 265	
tgg agc cag att cct cct gaa gac aca gca tcc acc cga tct tca ttc	1107
Trp Ser Gln Ile Pro Pro Glu Asp Thr Ala Ser Thr Arg Ser Ser Phe	
270 275 280	
act gtc caa gac ctt aaa cct ttt aca gaa tat gtg ttt agg att cgc	1155
Thr Val Gln Asp Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg Ile Arg	
285 290 295 300	
tgt atg aag gaa gat ggt aag gga tac tgg agt gac tgg agt gaa gaa	1203
Cys Met Lys Glu Asp Gly Lys Gly Tyr Trp Ser Asp Trp Ser Glu Glu	
305 310 315	

gca agt ggg atc acc tat gaa gat aga cca tct aaa gca cca agt ttc	1251
Ala Ser Gly Ile Thr Tyr Glu Asp Arg Pro Ser Lys Ala Pro Ser Phe	
320 325 330	
tgg tat aaa ata gat cca tcc cat act caa ggc tac aga act gta caa	1299
Trp Tyr Lys Ile Asp Pro Ser His Thr Gln Gly Tyr Arg Thr Val Gln	
335 340 345	
ctc gtg tgg aag aca ttg cct cct ttt gaa gcc aat gga aaa atc ttg	1347
Leu Val Trp Lys Thr Leu Pro Pro Phe Glu Ala Asn Gly Lys Ile Leu	
350 355 360	
gat tat gaa gtg act ctc aca aga tgg aaa tca cat tta caa aat tac	1395
Asp Tyr Glu Val Thr Leu Thr Arg Trp Lys Ser His Leu Gln Asn Tyr	
365 370 375 380	
aca gtt aat gcc aca aaa ctg aca gta aat ctc aca aat gat cgc tat	1443
Thr Val Asn Ala Thr Lys Leu Thr Val Asn Leu Thr Asn Asp Arg Tyr	
385 390 395	
cta gca acc cta aca gta aga aat ctt gtt ggc aaa tca gat gca gct	1491
Leu Ala Thr Leu Thr Val Arg Asn Leu Val Gly Lys Ser Asp Ala Ala	
400 405 410	
gtt tta act atc cct gcc tgt gac ttt caa gct act cac cct gta atg	1539
Val Leu Thr Ile Pro Ala Cys Asp Phe Gln Ala Thr His Pro Val Met	
415 420 425	
gat ctt aaa gca ttc ccc aaa gat aac atg ctt tgg gtg gaa tgg act	1587
Asp Leu Lys Ala Phe Pro Lys Asp Asn Met Leu Trp Val Glu Trp Thr	
430 435 440	
act cca agg gaa tct gta aag aaa tat ata ctt gag tgg tgt gtg tta	1635
Thr Pro Arg Glu Ser Val Lys Lys Tyr Ile Leu Glu Trp Cys Val Leu	
445 450 455 460	
tca gat aaa gca ccc tgt atc aca gac tgg caa caa gaa gat ggt acc	1683
Ser Asp Lys Ala Pro Cys Ile Thr Asp Trp Gln Gln Glu Asp Gly Thr	
465 470 475	
gtg cat cgc acc tat tta aga ggg aac tta gca gag agc aaa tgc tat	1731
Val His Arg Thr Tyr Leu Arg Gly Asn Leu Ala Glu Ser Lys Cys Tyr	
480 485 490	
ttg ata aca gtt act cca gta tat gct gat gga cca gga agc cct gaa	1779
Leu Ile Thr Val Thr Pro Val Tyr Ala Asp Gly Pro Gly Ser Pro Glu	
495 500 505	
tcc ata aag gca tac ctt aaa caa gct cca cct tcc aaa gga cct act	1827
Ser Ile Lys Ala Tyr Leu Lys Gln Ala Pro Pro Ser Lys Gly Pro Thr	
510 515 520	
gtt cgg aca aaa aaa gta ggg aaa aac gaa gct gtc tta gag tgg gac	1875
Val Arg Thr Lys Lys Val Gly Lys Asn Glu Ala Val Leu Glu Trp Asp	
525 530 535 540	
caa ctt cct gtt gat gtt cag aat gga ttt atc aga aat tat act ata	1923
Gln Leu Pro Val Asp Val Gln Asn Gly Phe Ile Arg Asn Tyr Thr Ile	
545 550 555	

ttt tat aga acc atc att gga aat gaa act gct gtg aat gtg gat tct	1971
Phe Tyr Arg Thr Ile Ile Gly Asn Glu Thr Ala Val Asn Val Asp Ser	
560 565 570	
tcc cac aca gaa tat aca ttg tcc tct ttg act agt gac aca ttg tac	2019
Ser His Thr Glu Tyr Thr Leu Ser Ser Leu Thr Ser Asp Thr Leu Tyr	
575 580 585	
atg gta cga atg gca gca tac aca gat gaa ggt ggg aag gat ggt cca	2067
Met Val Arg Met Ala Ala Tyr Thr Asp Glu Gly Gly Lys Asp Gly Pro	
590 595 600	
gaa ttc act ttt act acc cca aag ttt gct caa gga gaa att gaa gcc	2115
Glu Phe Thr Phe Thr Thr Pro Lys Phe Ala Gln Gly Glu Ile Glu Ala	
605 610 615 620	
ata gtc gtg cct gtt tgc tta gca ttc cta ttg aca act ctt ctg gga	2163
Ile Val Val Pro Val Cys Leu Ala Phe Leu Leu Thr Thr Leu Leu Gly	
625 630 635	
gtg ctg ttc tgc ttt aat aag cga gac cta att aaa aaa cac atc tgg	2211
Val Leu Phe Cys Phe Asn Lys Arg Asp Leu Ile Lys Lys His Ile Trp	
640 645 650	
cct aat gtt cca gat cct tca aag agt cat att gcc cag tgg tca cct	2259
Pro Asn Val Pro Asp Pro Ser Lys Ser His Ile Ala Gln Trp Ser Pro	
655 660 665	
cac act cct cca agg cac aat ttt aat tca aaa gat caa atg tat tca	2307
His Thr Pro Pro Arg His Asn Phe Asn Ser Lys Asp Gln Met Tyr Ser	
670 675 680	
gat ggc aat ttc act gat gta agt gtt gtg gaa ata gaa gca aat gac	2355
Asp Gly Asn Phe Thr Asp Val Ser Val Val Glu Ile Glu Ala Asn Asp	
685 690 695 700	
aaa aag cct ttt cca gaa gat ctg aaa tca ttg gac ctg ttc aaa aag	2403
Lys Lys Pro Phe Pro Glu Asp Leu Lys Ser Leu Asp Leu Phe Lys Lys	
705 710 715	
gaa aaa att aat act gaa gga cac agc agt ggt att ggg ggg tct tca	2451
Glu Lys Ile Asn Thr Glu Gly His Ser Ser Gly Ile Gly Gly Ser Ser	
720 725 730	
tgc atg tca tct tct agg cca agc att tct agc agt gat gaa aat gaa	2499
Cys Met Ser Ser Ser Arg Pro Ser Ile Ser Ser Ser Asp Glu Asn Glu	
735 740 745	
tct tca caa aac act tcg agc act gtc cag tat tct acc gtg gta cac	2547
Ser Ser Gln Asn Thr Ser Ser Thr Val Gln Tyr Ser Thr Val Val His	
750 755 760	
agt ggc tac aga cac caa gtt ccg tca gtc caa gtc ttc tca aga tcc	2595
Ser Gly Tyr Arg His Gln Val Pro Ser Val Gln Val Phe Ser Arg Ser	
765 770 775 780	
gag tct acc cag ccc ttg tta gat tca gag gag cgg cca gaa gat cta	2643
Glu Ser Thr Gln Pro Leu Leu Asp Ser Glu Glu Arg Pro Glu Asp Leu	
785 790 795	

caa tta gta gat cat gta gat ggc ggt gat ggt att ttg ccc agg caa	2691
Gln Leu Val Asp His Val Asp Gly Gly Asp Gly Ile Leu Pro Arg Gln	
800 805 810	
cag tac ttc aaa cag aac tgc agt cag cat gaa tcc agt cca gat att	2739
Gln Tyr Phe Lys Gln Asn Cys Ser Gln His Glu Ser Ser Pro Asp Ile	
815 820 825	
tca cat ttt gaa agg tca aag caa gtt tca tca gtc aat gag gaa gat	2787
Ser His Phe Glu Arg Ser Lys Gln Val Ser Ser Val Asn Glu Glu Asp	
830 835 840	
ttt gtt aga ctt aaa cag cag att tca gat cat att tca caa tcc tgt	2835
Phe Val Arg Leu Lys Gln Gln Ile Ser Asp His Ile Ser Gln Ser Cys	
845 850 855 860	
gga tct ggg caa atg aaa atg ttt cag gaa gtt tct gca gca gat gct	2883
Gly Ser Gly Gln Met Lys Met Phe Gln Glu Val Ser Ala Ala Asp Ala	
865 870 875	
ttt ggt cca ggt act gag gga caa gta gaa aga ttt gaa aca gtt ggc	2931
Phe Gly Pro Gly Thr Glu Gly Gln Val Glu Arg Phe Glu Thr Val Gly	
880 885 890	
atg gag gct gcg act gat gaa ggc atg cct aaa agt tac tta cca cag	2979
Met Glu Ala Ala Thr Asp Glu Gly Met Pro Lys Ser Tyr Leu Pro Gln	
895 900 905	
act gta cgg caa ggc ggc tac atg cct cag tga aggactagta gttcctgcta	3032
Thr Val Arg Gln Gly Gly Tyr Met Pro Gln	
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